MPRIMIKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARW   50

YEWLDPSIKKTEWSREEEEKLLHLAKLMPTQWRTIAPIIGRTAAQCLEHY   100

EFLLDKAAQRDNEEETTDDPRKLKPGEIDPNPETKPARPDPIDMDEDELE   150

MLSEARARLANTQGKKAKRKAREKQLEEARRLAALQKRRELRAAGIEIQK   200

KRKRKRGVDYNAEIPFEKKPALGFYDTSEENYQALDADFRKLRQQDLDGE   250

LRSEKEGRDRKKDKQHLKRKKESDLPSAILQTSGVSEFTKKRSKLVLPAP   300

QISDAELQEVVKVGQASEIARQTAEESGITNSASSTLLSEYNVTNNSVAL   350

RTPRTPASQDRILQEAQNLMALTNVDTPLKGGLNTPLHESDFSGVTPQRQ   400

VVQTPNTVLSTPFRTPSNGAEGLTPRSGTTPKPVINSTPGRTPLRDKLNI   450

NPEDGMADYSDPSYVKQMERESREHLRLGLLGLPAPKNDFEIVLPENAEK   500

ELEEREIDDTYIEDAADVDARKQAIRDAERVKEMKRMHKAVQKDLPRPSE   550

VNETILRPLNVEPPLTDLQKSEELIKKEMITMLHYDLLHHPYEPSGNKKG   600

KTVGFGTNNSEHITYLEHNPYEKFSKEELKKAQDVLVQEMEVVKQGMSHG   650

ELSSEAYNQVWEECYSQVLYLPGQSRYTRANLASKKDRIESLEKRLEINR   700

GHMTTEAKRAAKMEKKMKILLGGYQSRAMGLMKQLNDLWDQIEQAHLELR   750

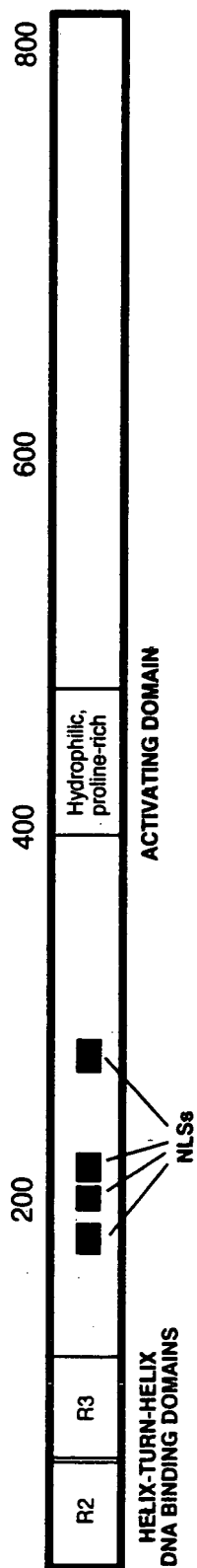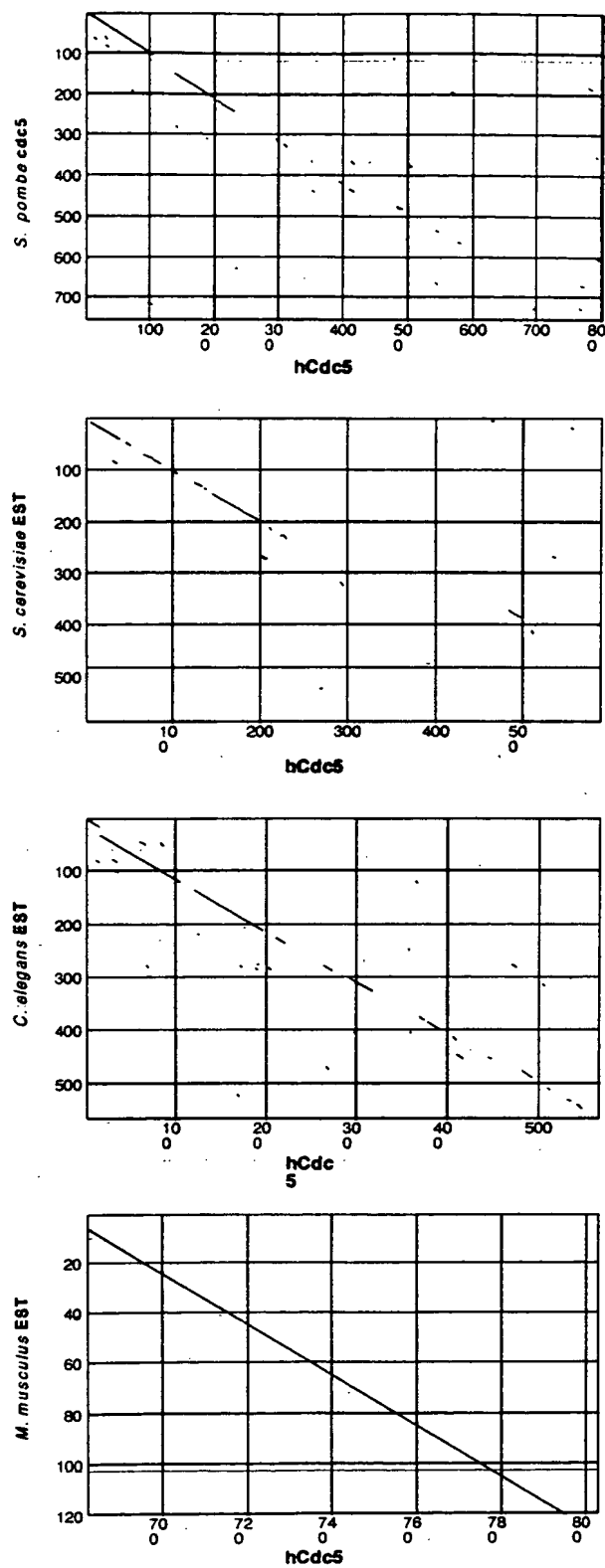TFEELKKHEDSAIPRRLECLKEDVQRQQEREKELQHRYADLLLEKETLKS   800

KF*

Fig. 1A

Fig. 1B

Fig. 2A

hCdc5	IKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARWYEWLDP	(6-56)
Spombe cdc5	LKGGAWKNTEDEILKAAVSKYGKNQWARISSLLVRKTPKQCKARWYEWIDP	(5-55)
b-Myb	VK-GPWTKEEDQKVIELVKKYGTKQWTLIAKHLKGRLGKQCRERWHNHLNP	(88-137)
a-Myb	IK-GPWTKEEDQRVIELVQKYGPKRWSLIAKHLKGRIGKQCRERWHNHLNP	(87-136)
c-Myb	IK-GPWTKEEDQRVIELVQKYGPKRWSVIAKHLKGRIGKQCRERWHNHLNP	(92-141)

Fig. 2B

hCdc5   PLKGGLNTPLHESDFSGVTPQRQVVQTPNTVLSTPFRTPSNGAEGLTPRSGTTPKPVINSTP (378-439)
S. pombe cdc5 SVTIEVRNQLMNREQSSLLGQESIPLQPGGTGYTGVT-PSHAANGS--ALAAP--Q--ATP (380-434)
b-Myb   PVK-TL--PFSPSQFLNFWNKQDTLELESPSLTSTPVCSQKVVVTTPLHRDKTPLHQKHAAF (445-503)
a-Myb   ILRKKRKMRVGHSPGSEL-RDGSLNDGGNMALKTPLKTPFSPSPSQFFNTCPGNEQLNIENPSF (446-508)

hCdc5   GRTPLRDKLNINPEDGMADYSDPSYVKQMERESREHLRLGLLGLPAPKNDFEIVLPENAEK (440-500)
S. pombe cdc5 FRTPR-DTFSINAAAERAGR-LASE-REN-KIRLKALRELLAKLPKPKNDYEL-ME-P-R- (435-487)
b-Myb   VTPDQKYSMDNTPHTP-TPFKNAKYGPLKPLPQTPHLEEDLKEVLRSEAGIELIIEDDIRP (504-565)
a-Myb   TSTPICGQKAL-ITTPLHKETTPKDQKENVGFRTPTIRRSILGTPRTPTPFKNALAAQEKK (509-569)

Fig. 2C

5' untranslated region:

```
GGCACGAGAGGAAGTGGCGGCTTTGAGTCCGGTGGCCCAATCGCTGTTACTACTTCTCTGAAGCTCCTCTCGGCTGCTTGC
CGAGACACCCTGCCGCCAAG
```

Coding region:

1 DNA BINDING DOMAIN (___)

```
   1 atgcctcgaa ttatgatcaa gggggggcgta tggaggaata ccgaggatga aattctgaaa
  61 gcagcggtaa tgaaatatgg gaaaaatcag tggtctagga ttgcctcatt gctgcataga
 121 aaatcagcaa agcagtgcaa agccagatgg tatgaatggc tggatccaag cattaagaag
 181 acagaatggt ccagagaaga agaggaaaaa ctcttgcact tggccaagtt gatgccaact
 241 cagtggagga ccattgctcc aatcattgga agaacagcgg cccagtgctt agaacactat
 301 gaatttcttc tggataaagc tgcccaaaga gacaatgaag aggaaacaac agatgatcca
 361 cgaaaactta aacctggaga aatagatcca aatccagaaa caaaaccagc gcggcctgat
 421 ccaattgata tggatgagga tgaacttgag atgctttctg aagccagagc ccgcttggct
```

2   NUCLEAR LOCALIZATION DOMAIN (___)

```
 481 aatactcagg gaaagaaggc caagaggaaa gcaagagaga acaattgga agaagcaaga
 541 cgtcttgctg ccctccaaaa aagaagagaa cttcgagcag ctggcataga aattcagaag
 601 aaaagaaaaa ggaagagagg agttgattat aatgccgaaa tcccatttga aaaaaagcct
 661 gcccttggtt tttatgatac ttctgaggaa aactaccaag ctcttgacgc agatttcagg
 721 aaattaagac aacaggatct tgatggggag ctaagatctg aaaaagaagg aagagataga
 781 aaaaaagaca aacagcattt gaaaaggaaa aaagaatctg atttaccatc agctattctt
 841 caaactagtg gtgtttctga atttactaaa aagagaagca aactagtact tcctgcccct
 901 cagatttcag atgcagaact ccaggaagtt gtaaaagtag gccaagcgag tgaaattgca
 961 cgtcaaactg ccgaggaatc tggcataaca aattctgctt ccagtacact tttgtctgag
1021 tacaatgtca ccaacaacag cgttgctctt agaacaccac gaacaccagc ttcccaggac
1081 agaattctgc aggaagccca gaacctcatg gccctcacca atgtggacac cccattgaaa
```

3   ACTIVATING DOMAIN   (___)

```
1141 ggtggactta atacccccatt gcatgagagt gacttctcag gtgtaactcc acagcgacaa
1201 gttgtacaga ctccaaacac agttctctct actccattca ggactccttc taatggagct
1261 gaagggctga ctccccggag tggaacaact cccaaaccag ttattaactc tactccgggt
1321 agaactcctc ttcgagacaa gttaaacatt aatcccgagg atggaatggc agactatagt
1381 gatccctctt acgtgaagca gatggaaaga gaatcccgag aacatctccg tttagggttg
1441 ttgggccttc ctgcccctaa gaatgatttt gaaattgttc taccagaaaa tgccgagaag
1501 gagctggaag aacgtgaaat agatgatact tacattgaag atgctgctga tgtggatgct
1561 cgaaagcagg ccatacgaga tgcagagcgt gtaaaggaaa tgaaacgaat gcataaagct
1621 gtccagaaag atctgccaag accatcagaa gtaaatgaaa ctattctaag acccttaaat
1681 gtagaaccgc ctttaacaga tttacagaaa agtgaagaac taatcaaaaa agaaatgatc
1741 acaatgcttc attatgacct tctacatcac ccttatgaac catctggaaa taaaaaaggc
1801 aaaactgtag ggtttggtac caataattca gagcacatta cctatctgga acataatcct
1861 tatgaaaagt tctccaaaga agagctgaaa aaggcccagg atgttttggt gcaggagatg
1921 gaagtggtta aacaaggaat gagccatgga gagctctcaa gtgaagctta taaccaggtg
1981 tgggaagaat gctacagtca agttttatat cttcctgggc agagccgcta cacacgggcc
2041 aatctggcta gtaaaaagga cagaattgaa tcacttgaaa agaggctcga gataaacagg
2101 ggtcacatga cgacagaagc caagagggct gcaaagatgg aaaagaagat gaaaattttg
2161 cttgggggt accagtctcg tgctatgggg ctcatgaaac agttgaatga cttatgggac
2221 caaattgaac aggctcactt ggagttacgc acttttgaag aactcaagaa acatgaagat
2281 tctgctattc cccggaggct agagtgtcta aaagaagacg ttcagcgaca acaagaaaga
2341 gaaaaggaac ttcaacatag atatgctgat ttgctgctgg agaaagagac tttaaagtca
2401 aaattctga
```

untranslated region:

```
AGTACAGTTTATATTCTGTCACAGGATTAATTAATTGCCGGTTTTCATACTCTAGAAGGCTGAAACTG ATGTTTATCTTCATTGACA
AATTTACCCACCATCTGTGGTTTTTCAGTTGTTTATTTTAAATGATATCGATCTTACACATTCTGTGTATAAAGACCTTAACTCCACA
GGACGGACATTTTAGAGTTTAAATTATTA AGGCTATCATTCTTTTAGTAAAAACAAAATATAAAAA
TTTAAAAAGCCTAATTTTAAAGTGCTGCCTGTGAGTAACTCTTGAATAAAAACAAAATATAAAAA
```
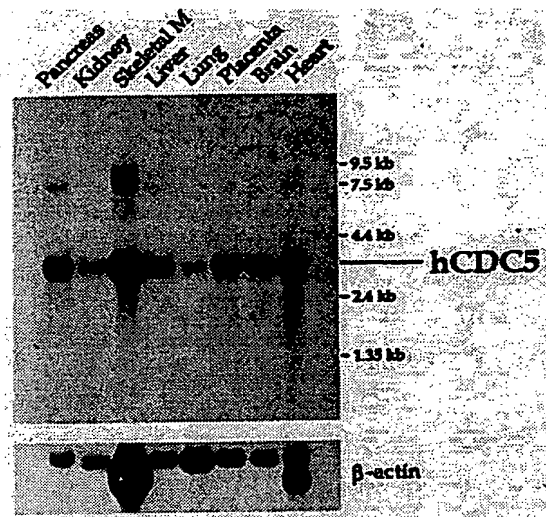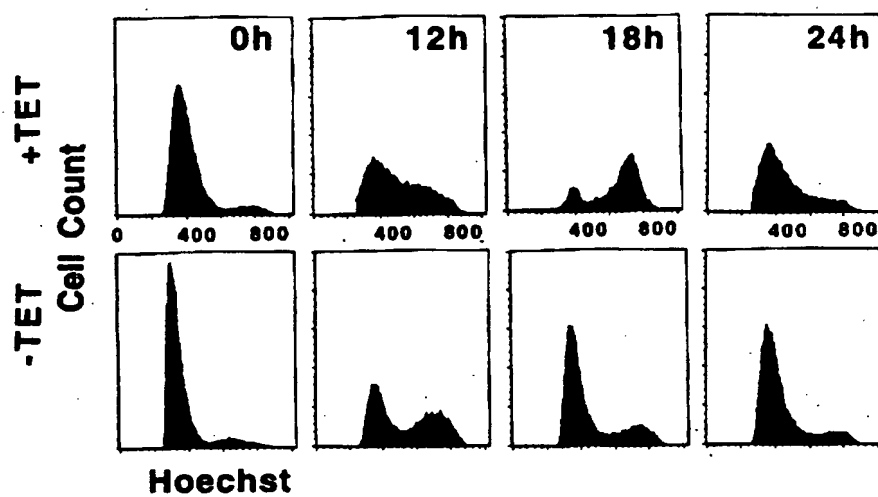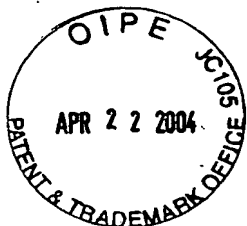
Fig. 2D
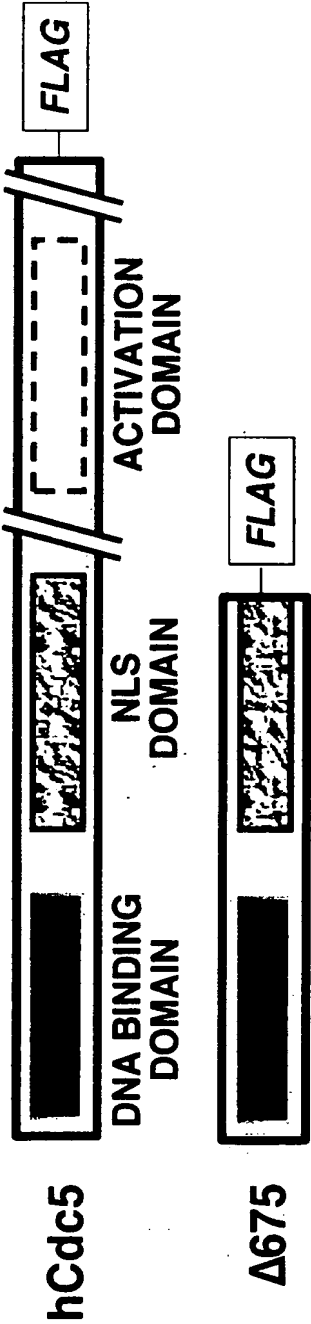
FIG. 3

FIG. 4A

FIG. 4B

FIG. 5
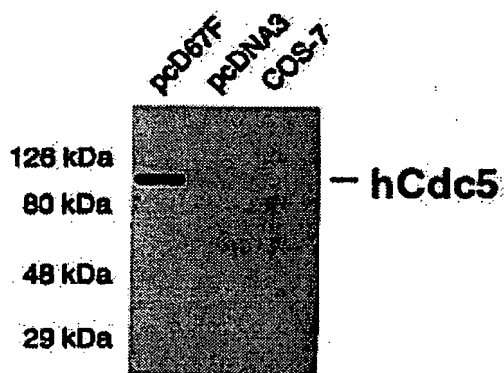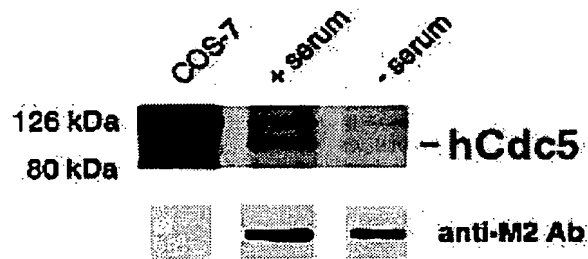
Fig. 6
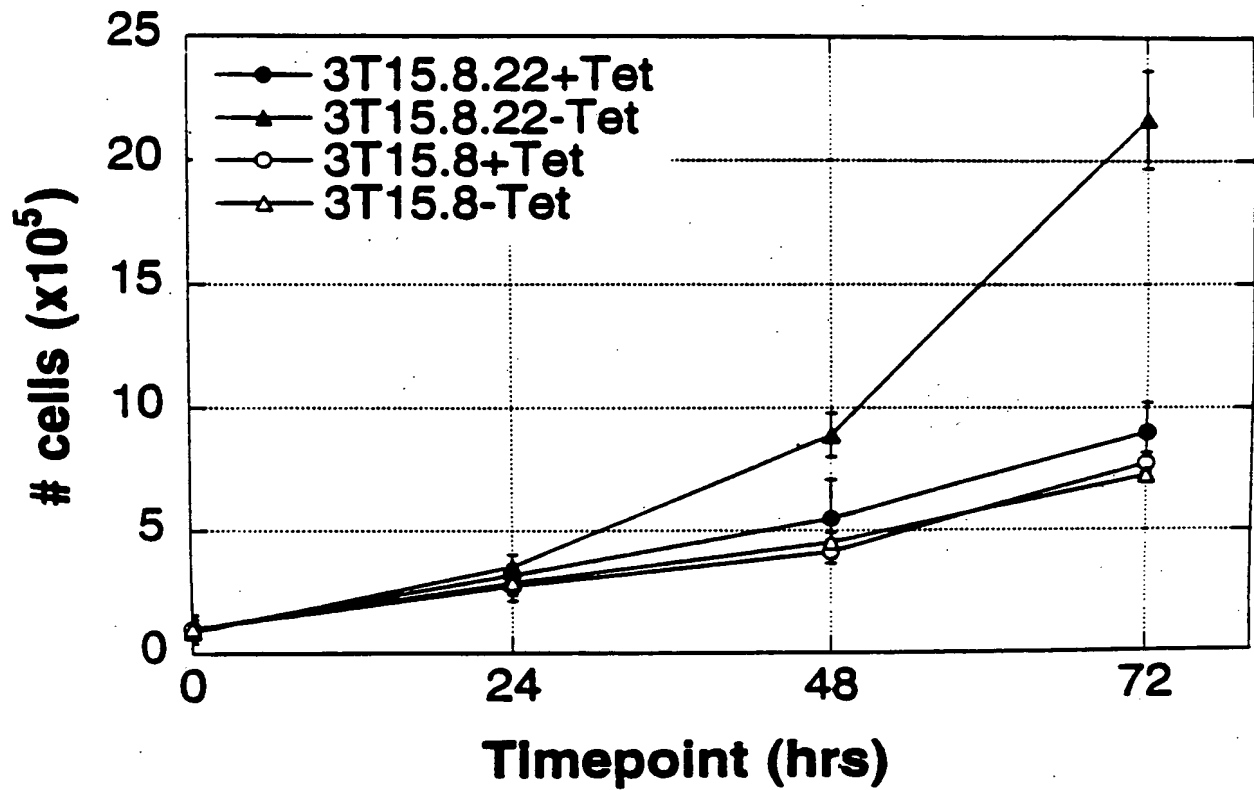
Fig. 7
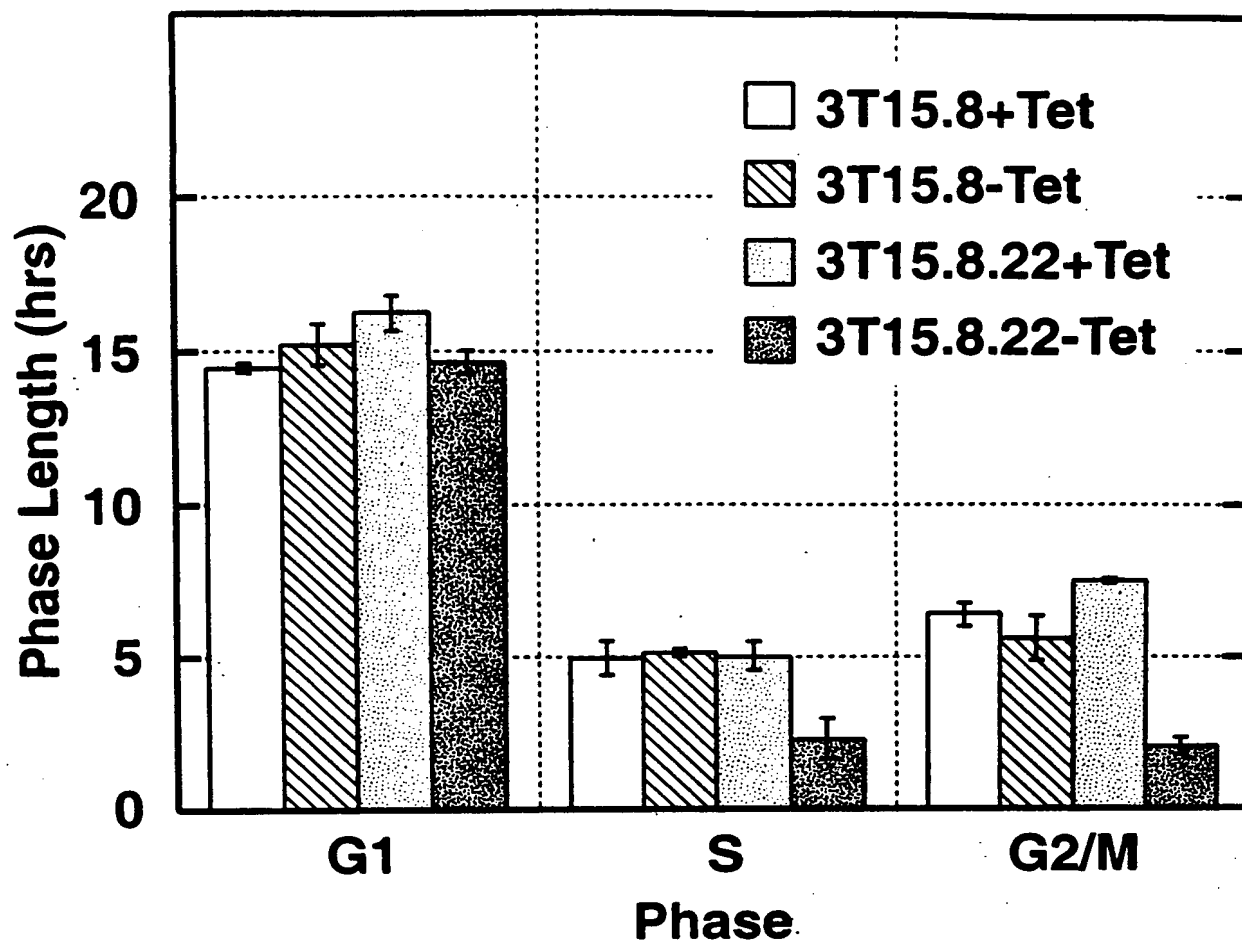
FIG. 8
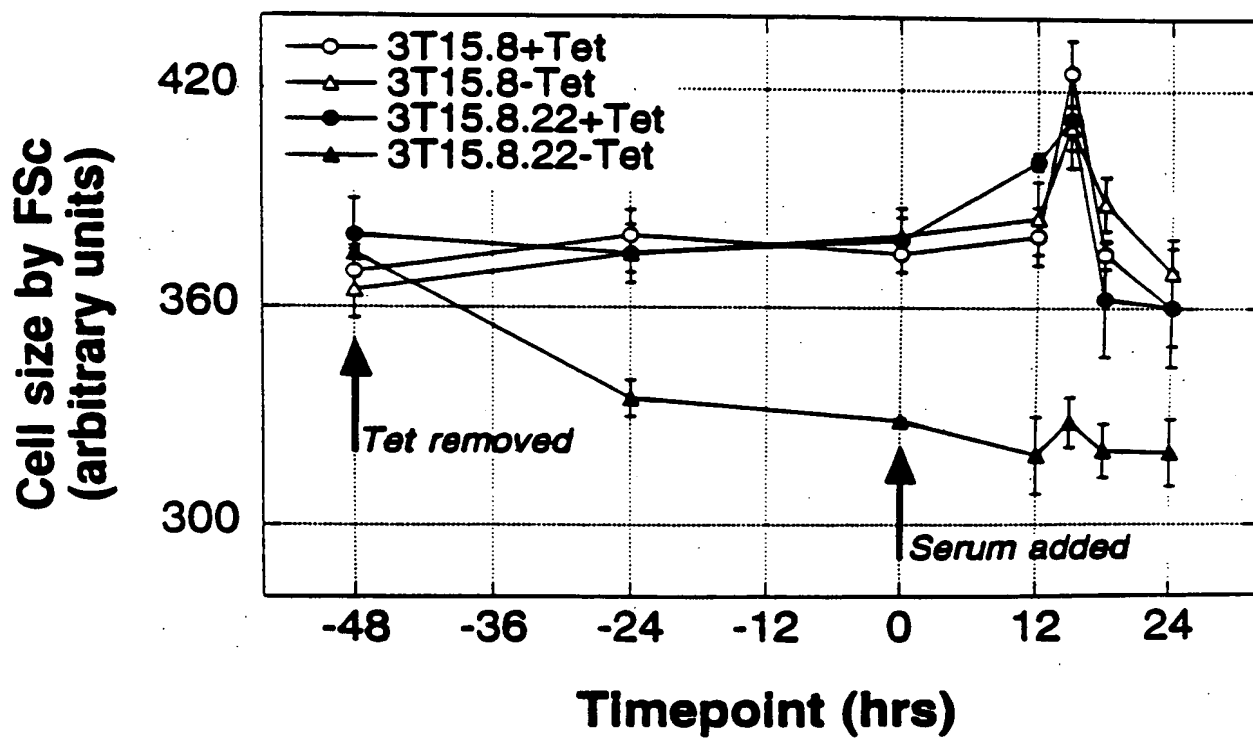
Fig. 9

Fig. 10

FIG. 11

Fig. 12

Fig. 13

0   12   15   18   21 hrs

hCdc5

p50 CLNE

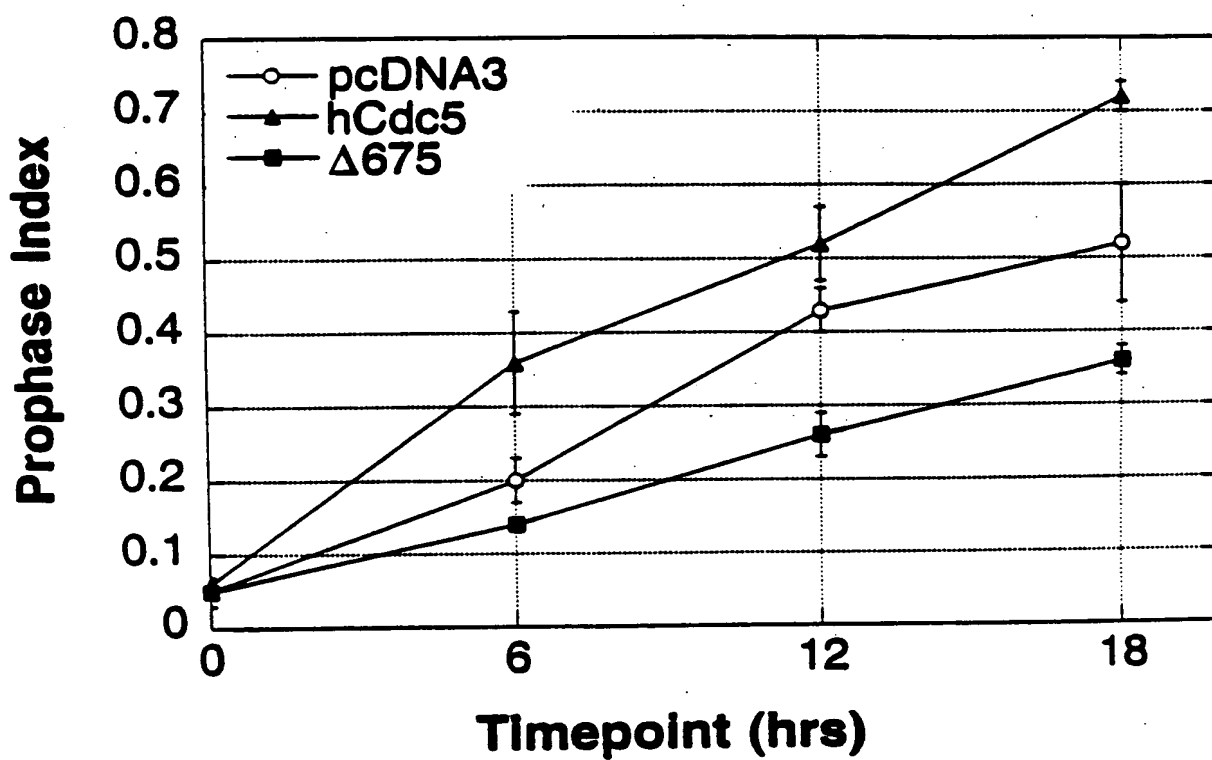p60 CLNA

p62 CLNB1
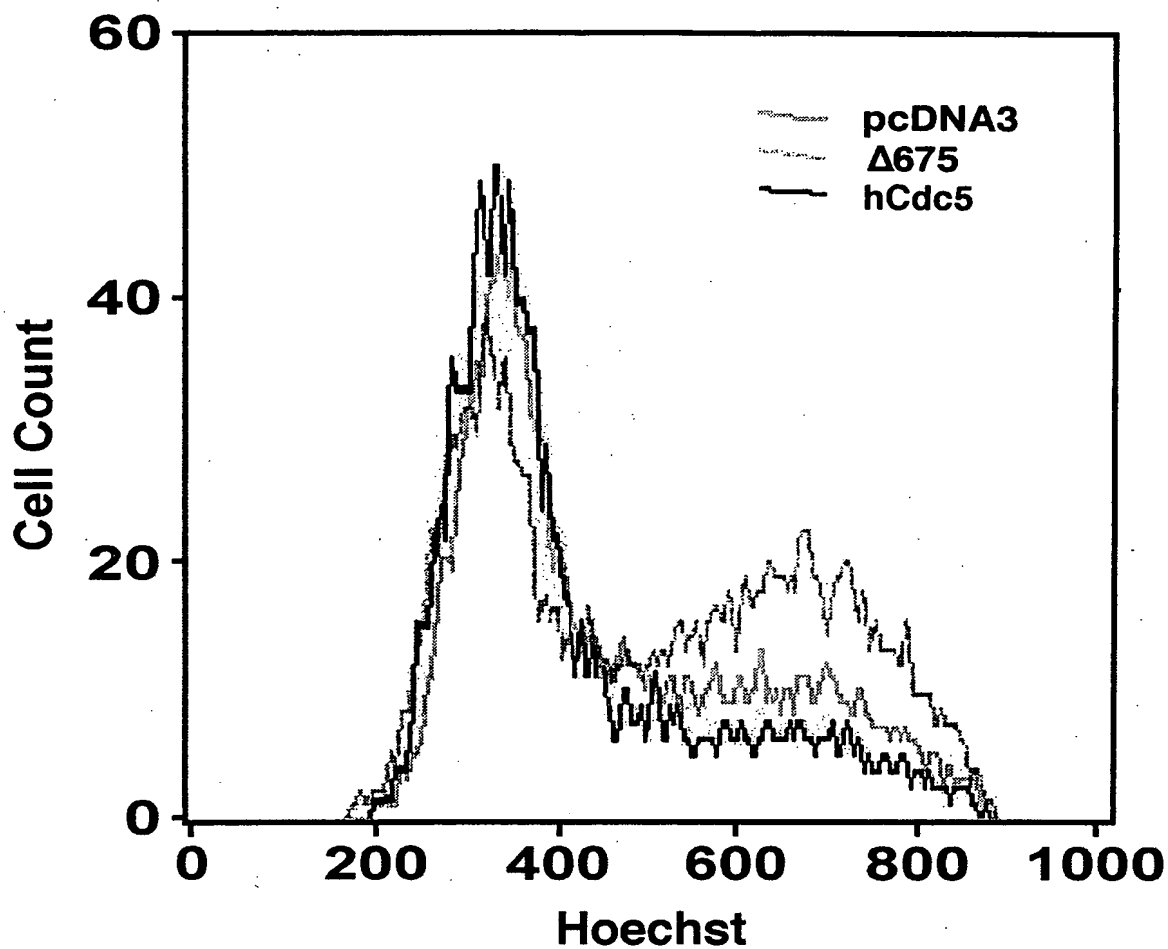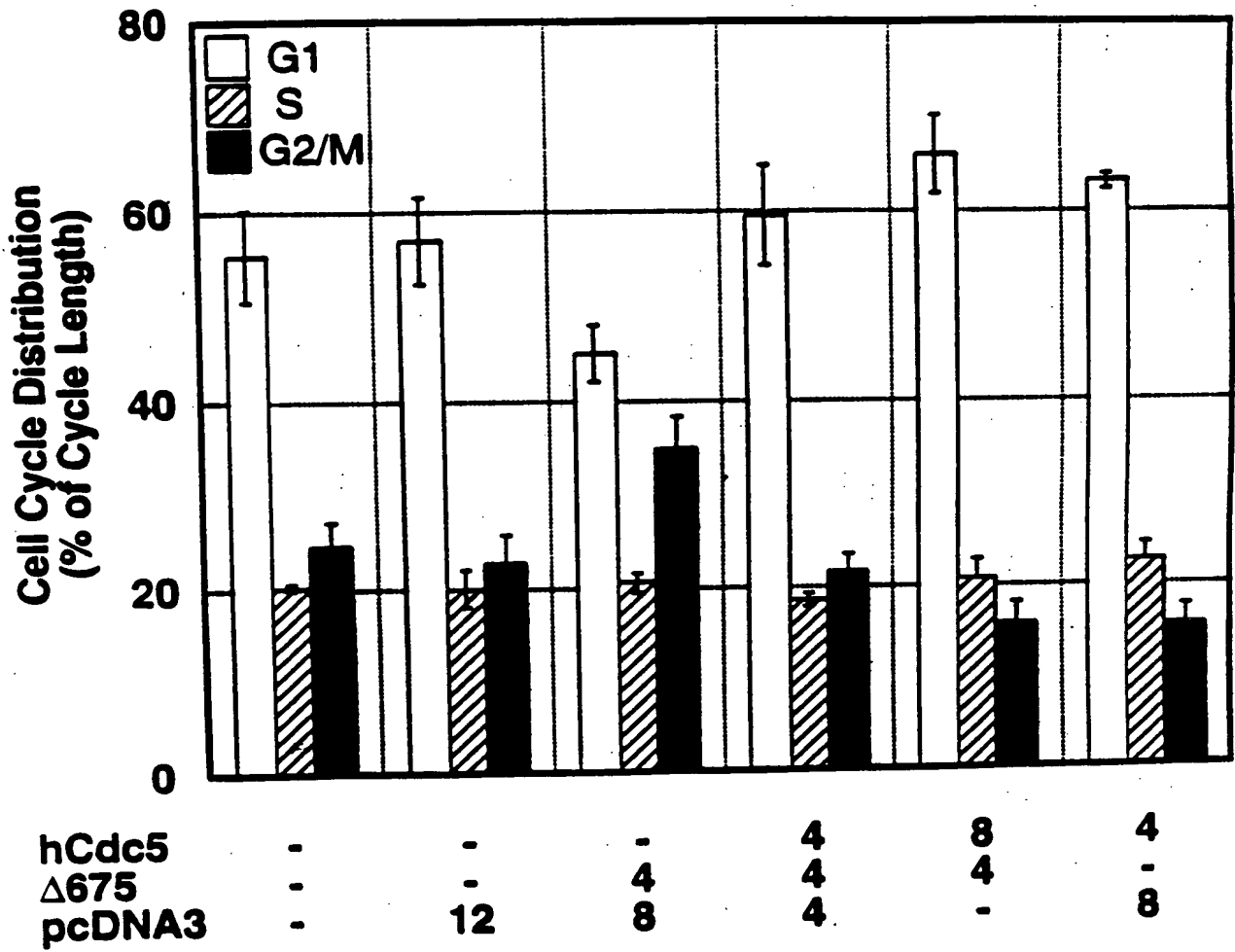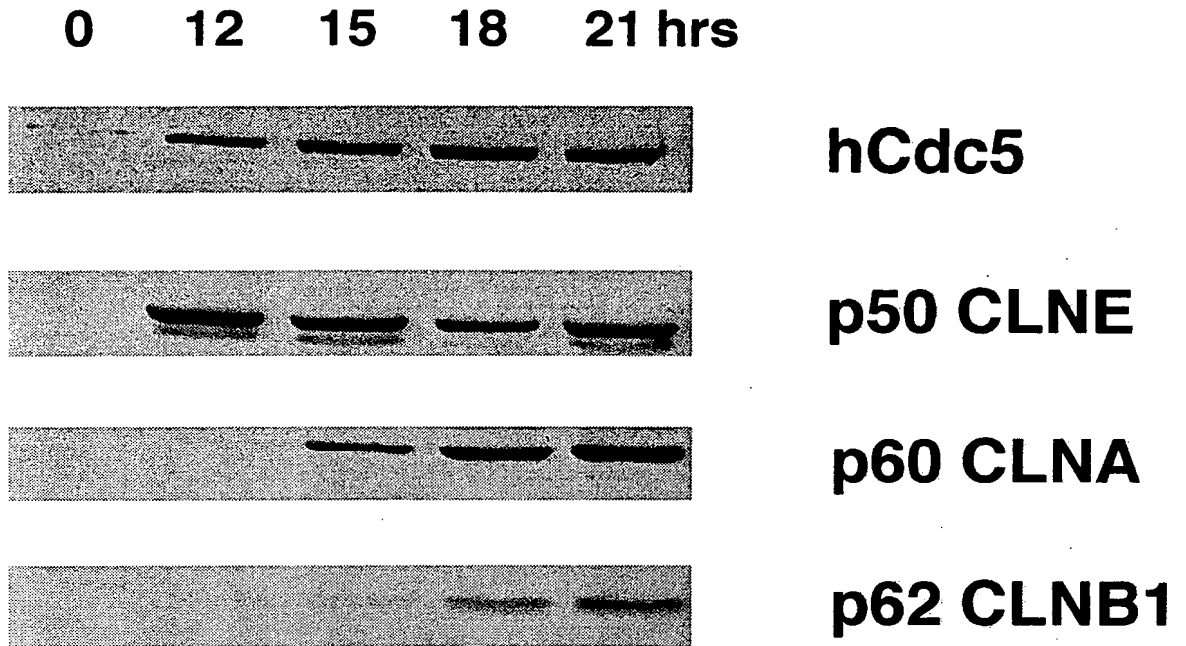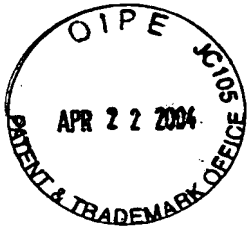
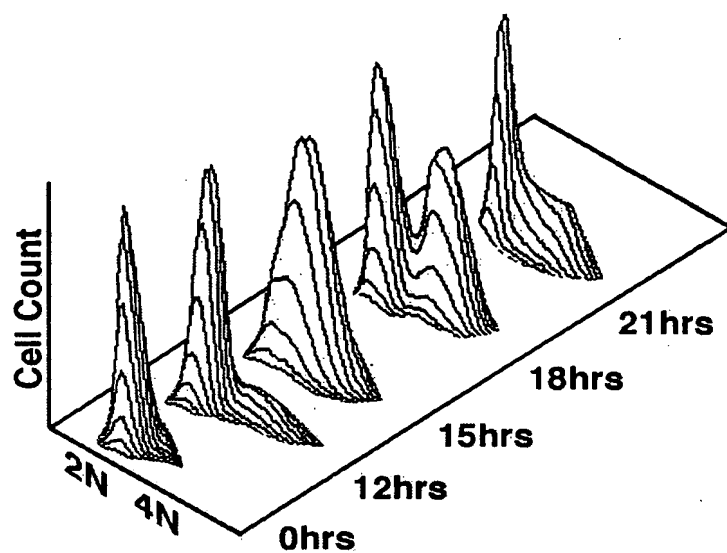**FIG. 14A**

FIG. 14B

```
Consensus      G A T T T A A C A T A A      (SEQ ID NO:13)

8.05           G A T T T A A C A T A A
8.04           G A T T T A A C A T A A
8.03           G A T T T A A C A T A A
8.02           G A T T T A A C A T A A
8.01           G A T T T A A C A T A A


6.05           G G T G T A A C G T G G      (SEQ ID NO:36)
6.04           G T G T T A C C A C A T      (SEQ ID NO:37)
6.03           C C A T A A T T T A G        (SEQ ID NO:38)
6.02           G A G A T A A A G T C T      (SEQ ID NO:39)
6.01           G T G T T A T T G A A A      (SEQ ID NO:40)


3.05           A C C C A C G T C T A T      (SEQ ID NO:41)
3.04           G G T T A G G A T A G G      (SEQ ID NO:42)
3.03           G T T G A G T A G T A T      (SEQ ID NO:43)
3.02           C T G T T A A T T T C C      (SEQ ID NO:44)
3.01           G G T G T T A T T G A T      (SEQ ID NO:45)
```

FIG 15